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SEQUENCE LISTING

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<120> METHODS OF CONFERRING PPO-INHIBITING HERBICIDE RESISTANCE IN PLANTS BY GENE MANIPULATION

<130> 2185-156P

<140> US 09/331,723

<141> 1999-08-18

<150> PCT/US96/20415

<151> 1996-12-27

<160> 24

<170> PatentIn version 3.0

<210> 1

<211> 47

<212> PRT

<213> Chlamydomonas reinhardtii

<220>

<221> misc\_feature

<222> ()..()

<223> Strain CC-407

<220>

<221> PEPTIDE

<222> (1)..(47)

<223> product = porphyric herbicide resistance domain

<400> 1

Ala Ala Glu Ala Leu Gly Ser Phe Asp Tyr Pro Pro Val Gly Ala Val  
1 5 10 15

Thr Leu Ser Tyr Pro Leu Ser Ala Val Arg Glu Glu Arg Lys Ala Ser  
20 25 30

Asp Gly Ser Val Pro Gly Phe Gly Gln Leu His Pro Arg Thr Gln  
35 40 45

<210> 2

<211> 46

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> misc\_feature  
<222> ()..()  
<223> ecotype Columbia

<220>  
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<222> (1)..(46)  
<223> product = porphyric herbicide resistance domain

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Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val  
1 5 10 15

Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp  
20 25 30

Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln  
35 40 45

<210> 3  
<211> 46  
<212> PRT  
<213> Zea mays

<220>  
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<222> ()..()  
<223> Strain B73 inbred

<220>  
<221> PEPTIDE  
<222> (1)..(46)  
<223> product = porphyric herbicide resistance domain

<400> 3

Ala Ala Asp Ala Leu Ser Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val  
1 5 10 15

Thr Val Ser Tyr Pro Lys Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp  
20 25 30

Gly Glu Leu Gln Gly Phe Gly Gln Leu His Pro Arg Ser Gln  
35 40 45

<210> 4  
<211> 141  
<212> DNA  
<213> Chlamydomonas reinhardtii

<220>  
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<222>  ()..()
<223> Strain CC-407

<220>
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<222> (1)..(141)
<223> encodes porphyric herbicide resistance domain

<400> 4
gcccggcagg ccctgggctc ctgcactac cgcgggtgg ggcgtgac gctgtcgta 60
ccgctgagcg ccgtgcggga ggagcgcaag gcctcgacg ggtccgtgcc gggcttcgg 120
cagctgcacc cgcgacgca g 141

<210> 5
<211> 138
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> ()..()
<223> ecotype Columbia

<220>
<221> misc_feature
<222> (1)..(138)
<223> encodes porphyric herbicide resistance domain

<400> 5
gctgcaaatg cactctcaaa actatattac ccaccagttt cagcagtatc tatctcgta 60
ccgaaagaag caatccgaac agaatgtttt atagatggtg aactaaaggg ttttggcaa 120
ttgcatccac gcacgcaa 138

<210> 6
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<212> DNA
<213> Zea mays

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<223> Strain B73 inbred

<220>
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<222> (1)..(138)

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<223> encodes porphyric herbicide resistance domain

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ccaaaggaag caatttagaaa agaatgctta attgatgggg aactccaggg ctttggccag 120  
ttgcatccac gtagtcaa 138

<210> 7  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
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<222> (1)..(36)  
<223> Oligonucleotide primer for Arabidopsis thaliana

<400> 7  
ctatattacc caccaatggc agcagtatct atctcg 36

<210> 8  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
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<222> (1)..(38)  
<223> Oligonucleotide primer for Zea mays

<400> 8  
gattctatta tccaccgatg gctgctgtaa ctgtttcg 38

<210> 9  
<211> 26  
<212> PRT  
<213> Artificial Sequence

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<222> ()..()  
<223> Oligonucleotide primer common to both of A. thaliana and Z. mays  
p

<220>  
<221> misc\_feature  
<222> ()..()  
<223> "n" residues can be inosine in addition to G, A, T or C; "k" at p

o

<400> 9

Lys Ala Tyr Thr Ala Tyr Cys Cys Asn Cys Cys Asn Ala Thr Gly Gly  
1 5 10 15

Ser Asn Gly Cys Asn Gly Thr Asn Trp Ser  
20 25

<210> 10

<211> 2573

<212> DNA

<213> Chlamydomonas reinhardtii

<220>

<221> misc\_feature

<222> ()..()

<223> Strain RS-3

<220>

<221> misc\_feature

<222> (1)..(2573)

<223> encodes protoporphyrinogen oxidase

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acgtccccct ttcctgtcac ccgtcccccc cggcgtttac tgcccttcc actcctcgcc 120

tccatcccga ttccatccgc tcctcctccc ccacctagac tgtctaccgt ctaccagtt 180

cttgggcaat cattaacgta accccgcctc cctgcgcctg ccctccctc cctctcccc 240

ccgcacagcc cgccgcccgc gaggccctgg gtccttcga ctacccgccg atgggcgccg 300

tgacgctgtc gtacccgtc agcgcgtgc gggaggagcg caaggcctcg gacgggtccg 360

tgccgggctt cggtcagctg cacccgcgca cgcaggtggg caagtgcgcg cgtgttgcgg 420

gcggtgtgtt gcggaggggaa ggggtgggg gggtgggggt ggggtgggg gggattgggg 480

cgcgtggctcg tatccgcgg ttgtatcctc gcgcctccct catccattcc ccccttcaac 540

aacacacacg ggccgcacacg caccctcttt gcgcctactt tgtctggtgc tccttaacac 600

actttcgct tcatttttgtt gtcttctaac acacacactt gtccacacac agggcatcac 660

cactctgggc accatctaca gctccagcct gttcccgcc cgccgcggc agggccacat 720

gcgtgcgtgc aaciacaacy gcygcacccac caacccggc aicgcdaacc ayaccacca 780

gcagctggtg gagcaggtgt gtgtgtgggg ggggtgggggg ggggcagtgg atttttggc 840

tgagccccct gagcaaagcg atccaggggg ggcgaagccc cccaggatty cccctgtccg	900
tgcgtgcgtg tgtgcctgtg tcgacaaaaaa gtaccgtact ggcacaaacc gcgagtgcc	960
cgtattatta attgcaatta cctattgttag aaaaatagac ggcagggaaa actcgccgg	1020
agcgagaagc gacctcgtga gtccatggac atcttgcatt tcttcagttc gcgagttatag	1080
ctctcgcccc ctaaatatct tacatccatg tatcaaaaca tgtcgacgac aagcgtctt	1140
gggcaagaat gtcgaaattt tttgcaacag ccaaaccatg cgtccccgag ccttacatgt	1200
gtcgcccccc gggatcccgc gcccggcccc ggctagccct ttgcgggtct tgagtggat	1260
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cgtggccccg acagggcatg tcgggtccctc ggcacagcgt tggcttagtgc gccagtcgg	1380
ctggatgggc ttgcaagggt gctgttcatg tcgccccgtc ccatcgtaac atcccattgc	1440
gctacatggg gctcagccca ttttccagct gtacaaagct gacacccctt gttgtgtggc	1500
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cacacacaca cacacacaca cacacacaca cacacacaca cacacacaca	1620
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ccgaaccccg ccgccccgttc cacgtttcc acctggcga ccccccccccc tgccgcacgc	1740
ctgctctcac cgccctctccc cccacccat ctccctgcag gtggacaagg acctgcgcaa	1800
catggtcatac aagcccacg cgcccaagcc ccgtgtggt ggcgtgcgcg tgtggccgcg	1860
cgcacatcccg caggtgtgag ggcgcagcag ccggagggat gggctagatc ctgtttctc	1920
aaagagctct acagccctat aacctcgacc tgcgacccctc gacctgataa cctggctgcc	1980
ccctcccaac cttagccacct ctccccggat ttgggttac tgcgttgact tgctttggg	2040
ttcttggaaatc aacttcacact gttgtataact ttgcgtgcact tctctgtacc actctttgca	2100
ttaggttcgg ttttagttgg gctgcatagtg taacccctcc tccccggccct gccacctgca	2160
gttcaacctg ggccacctgg agcagctggca caaggcgcgc aaggcgtgg acgcggcggg	2220
gctgcagggc gtgcacctgg ggggcaacta cgtcagcggt gagcgcgtgg gcagcagcag	2280
cagcaggaag aggggagggg aggggagggg agggtacaag gaggaggtt agcaggaggt	2340
ggtgctaagg cgcaaagcaa ggcgggtttg tatcctcatt gactgaaacc gggaaaccca	2400
gcatgaacaa gaggtcaggg gactgcaagg agcggaggct acatgtatga ctaccccgaa	2460
cgccggcgat gattccttga ctattggac ctattcggtt gggctcgggc acatgacccc	2520
cctggccccct tcgctgtatg gtgcccagcc gcccagccgc ccccccggccca cac	2573

<210> 11  
 <211> 1704  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> ecotype Columbia

<220>  
 <221> CDS  
 <222> (16)..(1629)  
 <223> product = protoporphyrinogen oxidase

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1              5                    10		
cct ctt ccg tcg ttt tcg aag ccc aat ctc cga tta aat gtt tat aag		99
Leu Leu Pro Ser Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys		
15            20                    25		
cct ctt aga ctc cgt tgt tca gtg gcc ggt gga cca acc gtc gga tct		147
Pro Leu Arg Leu Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser		
30            35                    40		
tca aaa atc gaa ggc gga gga ggc acc acc atc acg acg gat tgt gtg		195
Ser Lys Ile Glu Gly Gly Thr Thr Ile Thr Thr Asp Cys Val		
45            50                    55                    60		
att gtc ggc gga ggt att agt ggt ctt tgc atc gct cag gcg ctt gct		243
Ile Val Gly Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala		
65            70                    75		
act aag cat cct gat gct gct ccg aat tta att gtg acc gag gct aag		291
Thr Lys His Pro Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys		
80            85                    90		
gat cgt gtt gga ggc aac att atc act cgt gaa gag aat ggt ttt ctc		339
Asp Arg Val Gly Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu		
95            100                    105		
tgg gaa gaa ggt ccc aat agt tttcaa ccg tct gat cct atg ctc act		387
Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr		
110            115                    120		
atg gtg gta gat agt ggt ttg aag gat gat ttg gtg ttg gga gat cct		435
Met Val Val Asp Ser Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro		
125            130                    135                    140		
act gcg cca agg ttt gtg ttg aat ggg aaa ttg agg ccg gtt cca		483

Thr Ala Pro Arg Phe Val Leu Trp Asn Gly Lys Leu Arg Pro Val Pro			
145	150	155	
tcg aag cta aca gac tta ccg ttc ttt gat ttg atg agt att ggt ggg		531	
Ser Lys Leu Thr Asp Leu Pro Phe Asp Leu Met Ser Ile Gly Gly			
160	165	170	
aag att aga gct ggt ttt ggt gca ctt ggc att cga ccg tca cct cca		579	
Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Ser Pro Pro			
175	180	185	
ggt cgt gaa gaa tct gtg gag gag ttt gta ccg cgt aac ctc ggt gat		627	
Gly Arg Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly Asp			
190	195	200	
gag gtt ttt gag cgc ctg att gaa ccg ttt tgt tca ggt gtt tat gct		675	
Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala			
205	210	215	220
ggt gat cct tca aaa ctg agc atg aaa gca gcg ttt ggg aag gtt tgg		723	
Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp			
225	230	235	
aaa cta gag caa aat ggt gga agc ata ata ggt ggt act ttt aag gca		771	
Lys Leu Glu Gln Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala			
240	245	250	
att cag gag agg aaa aac gct ccc aag gca gaa cga gac ccg cgc ctg		819	
Ile Gln Glu Arg Lys Asn Ala Pro Lys Ala Glu Arg Asp Pro Arg Leu			
255	260	265	
cca aaa cca cag ggc caa aca gtt ggt tct ttc agg aag gga ctt cga		867	
Pro Lys Pro Gln Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg			
270	275	280	
atg ttg cca gaa gca ata tct gca aga tta ggt agc aaa gtt aag ttg		915	
Met Leu Pro Glu Ala Ile Ser Ala Arg Leu Gly Ser Lys Val Lys Leu			
285	290	295	300
tct tgg aag ctc tca ggt atc act aag ctg gag agc gga gga tac aac		963	
Ser Trp Lys Leu Ser Gly Ile Thr Lys Leu Glu Ser Gly Gly Tyr Asn			
305	310	315	
tta aca tat gag act cca gat ggt tta gtt tcc gtg cag agc aaa agt		1011	
Leu Thr Tyr Glu Thr Pro Asp Gly Leu Val Ser Val Gln Ser Lys Ser			
320	325	330	
gtt gta atg acg gtg cca tct cat gtt gca agt ggt ctc ttg cgc cct		1059	
Val Val Met Thr Val Pro Ser His Val Ala Ser Gly Leu Leu Arg Pro			
335	340	345	
ctt tct gaa tct gct gca aat gca ctc tca aaa cta tat tac cca cca		1107	
Leu Ser Glu Ser Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro			
350	355	360	
gtt gca gca gta tct atc tcg tac ccg aaa gaa gca atc cga aca gaa		1155	
Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu			

365	370	375	380	
tgt ttg ata gat ggt gaa cta aag ggt ttt ggg caa ttg cat cca cgc Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg 385 390 395				1203
acg caa gga gtt gaa aca tta gga act atc tac agc tcc tca ctc ttt Thr Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe 400 405 410				1251
cca aat cgc gca ccg ccc gga aga att ttg ctg ttg aac tac att ggc Pro Asn Arg Ala Pro Pro Gly Arg Ile Leu Leu Asn Tyr Ile Gly 415 420 425				1299
ggg tct aca aac acc gga att ctg tcc aag tct gaa ggt gag tta gtg Gly Ser Thr Asn Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val 430 435 440				1347
gaa gca gtt gac aga gat ttg agg aaa atg cta att aag cct aat tcg Glu Ala Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser 445 450 455 460				1395
acc gat cca ctt aaa tta gga gtt agg gta tgg cct caa gcc att cct Thr Asp Pro Leu Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro 465 470 475				1443
cag ttt cta gtt ggt cac ttt gat atc ctt gac acg gct aaa tca tct Gln Phe Leu Val Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser 480 485 490				1491
cta acg tct tcg ggc tac gaa ggg cta ttt ttg ggt ggc aat tac gtc Leu Thr Ser Ser Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val 495 500 505				1539
gct ggt gta gcc tta ggc cggttgt gta gaa ggc gca tat gaa acc acc gcg Ala Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Thr Ala 510 515 520				1587
att gag gtc aac aac ttc atg tca cgg tac gct tac aag taa Ile Glu Val Asn Asn Phe Met Ser Arg Tyr Ala Tyr Lys 525 530 535				1629
atgtaaaaca ttaaatctcc cagttgcgt gagtttatt aaatatttg agatatccaa aaaaaaaaaaaa aaaaa				1689
				1704

<210> 12  
 <211> 537  
 <212> PRT  
 <213> Arabidopsis thaliana  
  
 <220>  
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 <222> ()..()  
 <223> ecotype Columbia

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Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys Pro Leu Arg Leu  
20 25 30

Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser Ser Lys Ile Glu  
35 40 45

Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val Ile Val Gly Gly  
50 55 60

Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala Thr Lys His Pro  
65 70 75 80

Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys Asp Arg Val Gly  
85 90 95

Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu Trp Glu Glu Gly  
100 105 110

Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Val Val Asp  
115 120 125

Ser Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Thr Ala Pro Arg  
130 135 140

Phe Val Leu Trp Asn Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr  
145 150 155 160

Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Gly Gly Lys Ile Arg Ala  
165 170 175

Gly Phe Gly Ala Leu Gly Ile Arg Pro Ser Pro Pro Gly Arg Glu Glu  
180 185 190

Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly Asp Glu Val Phe Glu  
195 200 205

Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser  
210 215 220

Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Gln  
225 230 235 240

Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Gln Glu Arg  
245 250 255

Lys Asn Ala Pro Lys Ala Glu Arg Asp Pro Arg Leu Pro Lys Pro Gln  
260 265 270

Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Glu  
275 280 285

Ala Ile Ser Ala Arg Leu Gly Ser Lys Val Lys Leu Ser Trp Lys Leu  
290 295 300

Ser Gly Ile Thr Lys Leu Glu Ser Gly Gly Tyr Asn Leu Thr Tyr Glu  
305 310 315 320

Thr Pro Asp Gly Leu Val Ser Val Gln Ser Lys Ser Val Val Met Thr  
325 330 335

Val Pro Ser His Val Ala Ser Gly Leu Leu Arg Pro Leu Ser Glu Ser  
340 345 350

Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val  
355 360 365

Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp  
370 375 380

Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val  
385 390 395 400

Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala  
405 410 415

Pro Pro Gly Arg Ile Leu Leu Asn Tyr Ile Gly Gly Ser Thr Asn  
420 425 430

Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val Glu Ala Val Asp  
435 440 445

Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser Thr Asp Pro Leu  
450 455 460

Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val  
465 470 475 480

Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser Leu Thr Ser Ser  
485 490 495

Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ala Gly Val Ala  
500 505 510

Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Thr Ala Ile Glu Val Asn  
515 520 525

Asn Phe Met Ser Arg Tyr Ala Tyr Lys  
530 535

<210> 13  
<211> 1698  
<212> DNA  
<213> Zea mays

<220>  
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<223> Strain B73 inbred

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<223> product = protoporphyrinogen oxidase

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Asn Ser Ala Asp Cys Val Val Gly Gly Ile Ser Gly Leu Cys  
1 5 10 15

acc gcg cag gcg ctg gcc acg cgg cac ggc gtc ggg gac gtg ctt gtc 97  
Thr Ala Gln Ala Leu Ala Thr Arg His Gly Val Gly Asp Val Leu Val  
20 25 30

acg gag gcc cgc gcc ccc ggc aac att acc acc gtc gag cgc 145  
Thr Glu Ala Arg Ala Arg Pro Gly Gly Asn Ile Thr Val Glu Arg  
35 40 45

ccc gag gaa ggg tac ctc tgg gag gag ggt ccc aac agc ttc cag ccc 193  
Pro Glu Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro  
50 55 60

tcc gac ccc gtt ctc acc atg gcc gtg gac agc gga ctg aag gat gac			241
Ser Asp Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp			
65	70	75	80
 ttg gtt ttt ggg gac cca aac gcg ccg cgt ttc gtg ctg tgg gag ggg			289
Leu Val Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly			
85	90	95	
 aag ctg agg ccc gtg cca tcc aag ccc gcc gac ctc ccg ttc ttc gat			337
Lys Leu Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe Asp			
100	105	110	
 ctc atg agc atc cca ggg aag ctc agg gcc ggt cta ggc gcg ctt ggc			385
Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly			
115	120	125	
 atc cgcc ccg cct cct cca ggc cgcc gaa gag tca gtg gag gag ttc gtg			433
Ile Arg Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val			
130	135	140	
 cgcc cgcc aac ctc ggt gct gag gtc ttt gag cgcc ctc att gag cct ttc			481
Arg Arg Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe			
145	150	155	160
 tgc tca ggt gtc tat gct ggt gat cct tct aag ctc agc atg aag gct			529
Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala			
165	170	175	
 gca ttt ggg aag gtt tgg cgg ttg gaa gaa act gga ggt agt att att			577
Ala Phe Gly Lys Val Trp Arg Leu Glu Glu Thr Gly Gly Ser Ile Ile			
180	185	190	
 ggc gga acc atc aag aca att cag gag agg agc aag aat cca aaa cca			625
Gly Gly Thr Ile Lys Thr Ile Gln Glu Arg Ser Lys Asn Pro Lys Pro			
195	200	205	
 ccg agg gat gcc cgcc ctt ccg aag cca aaa ggg cag aca gtt gca tct			673
Pro Arg Asp Ala Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Ala Ser			
210	215	220	
 ttc agg aag ggt ctt gcc atg ctt cca aat gcc att aca tcc agc ttg			721
Phe Arg Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Thr Ser Ser Leu			
225	230	235	240
 ggc agt aaa gtc aaa cta tca tgg aaa ctc acg agc att aca aaa tca			769
Gly Ser Lys Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys Ser			
245	250	255	
 gat gac aag gca tat gtt ttg gag tat gaa acg cca gaa ggg gtt gtt			817
Asp Asp Lys Gly Tyr Val Leu Glu Tyr Glu Thr Pro Glu Gly Val Val			
260	265	270	
 tcg gtg cag gct aaa agt gtt atc atg act att cca tca tat gtt gct			865
Ser Val Gln Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val Ala			
275	280	285	

agc aac att ttg cgt cca ctt tca agc gat gct gca gat gct cta tca Ser Asn Ile Leu Arg Pro Leu Ser Ser Asp Ala Ala Asp Ala Leu Ser	913
290 295 300	
aga ttc tat tat cca ccg gtt gct gta act gtt tcg tat cca aag Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys	961
305 310 315 320	
gaa gca att aga aaa gaa tgc tta att gat ggg gaa ctc cag ggc ttt Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly Phe	1009
325 330 335	
ggc cag ttg cat cca cgt agt caa gga gtt gag aca tta gga aca ata Gly Gln Leu His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile	1057
340 345 350	
tac agt tcc tca ctc ttt cca aat cgt gct cct gac ggt agg gtg tta Tyr Ser Ser Leu Phe Pro Asn Arg Ala Pro Asp Gly Arg Val Leu	1105
355 360 365	
ctt cta aac tac ata gga ggt gct aca aac aca gga att gtt tcc aag Leu Leu Asn Tyr Ile Gly Gly Ala Thr Asn Thr Gly Ile Val Ser Lys	1153
370 375 380	
act gaa agt gag ctg gtc gaa gca gtt gac cgt gac ctc cga aaa atg Thr Glu Ser Glu Leu Val Glu Ala Val Asp Arg Asp Leu Arg Lys Met	1201
385 390 395 400	
ctt ata aat tct aca gca gtg gac cct tta gtc ctt ggt gtt cga gtt Leu Ile Asn Ser Thr Ala Val Asp Pro Leu Val Leu Gly Val Arg Val	1249
405 410 415	
tgg cca caa gcc ata cct cag ttc ctg gta gga cat ctt gat ctt ctg Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu	1297
420 425 430	
gaa gcc gca aaa gct gcc ctg gac cga ggt ggc tac gat ggg ctg ttc Glu Ala Ala Lys Ala Ala Leu Asp Arg Gly Gly Tyr Asp Gly Leu Phe	1345
435 440 445	
cta gga ggg aac tat gtt gca gga gtt gcc ctg ggc aga tgc gtt gag Leu Gly Gly Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Val Glu	1393
450 455 460	
ggc gcg tat gaa agt gcc tcg caa ata tct gac ttc ttg acc aag tat Gly Ala Tyr Glu Ser Ala Ser Gln Ile Ser Asp Phe Leu Thr Lys Tyr	1441
465 470 475 480	
gcc tac aag tga tgaaagaagt ggagcgctac ttgccaatcg tttatgttgc Ala Tyr Lys	1493
atacatgagg tgcctccggg gaaaaaaaaag cttgaatagt attttttatt cttatTTTGT	1553
aaattgcatt tctgttcttt ttcttatcag taatttagtta tatttttagtt ctgttaggaga	1613
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ctacttaaaa aaaaaaaaaa aaaaa

1698

<210> 14  
<211> 483  
<212> PRT  
<213> Zea mays

<220>  
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<223> Strain B73 inbred

<400> 14

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Thr Glu Ala Arg Ala Arg Pro Gly Gly Asn Ile Thr Thr Val Glu Arg  
35 40 45

Pro Glu Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro  
50 55 60

Ser Asp Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp  
65 70 75 80

Leu Val Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly  
85 90 95

Lys Leu Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe Asp  
100 105 110

Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly  
115 120 125

Ile Arg Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val  
130 135 140

Arg Arg Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe  
145 150 155 160

Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala

165

170

175

Ala Phe Gly Lys Val Trp Arg Leu Glu Glu Thr Gly Gly Ser Ile Ile  
180 185 190

Gly Gly Thr Ile Lys Thr Ile Gln Glu Arg Ser Lys Asn Pro Lys Pro  
195 200 205

Pro Arg Asp Ala Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Ala Ser  
210 215 220

Phe Arg Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Thr Ser Ser Leu  
225 230 235 240

Gly Ser Lys Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys Ser  
245 250 255

Asp Asp Lys Gly Tyr Val Leu Glu Tyr Glu Thr Pro Glu Gly Val Val  
260 265 270

Ser Val Gln Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val Ala  
275 280 285

Ser Asn Ile Leu Arg Pro Leu Ser Ser Asp Ala Ala Asp Ala Leu Ser  
290 295 300

Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys  
305 310 315 320

Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly Phe  
325 330 335

Gly Gln Leu His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile  
340 345 350

Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Asp Gly Arg Val Leu  
355 360 365

Leu Leu Asn Tyr Ile Gly Gly Ala Thr Asn Thr Gly Ile Val Ser Lys  
370 375 380

Thr Glu Ser Glu Leu Val Glu Ala Val Asp Arg Asp Leu Arg Lys Met  
385 390 395 400

Leu Ile Asn Ser Thr Ala Val Asp Pro Leu Val Leu Gly Val Arg Val  
405 410 415

Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu  
420 425 430

Glu Ala Ala Lys Ala Ala Leu Asp Arg Gly Gly Tyr Asp Gly Leu Phe  
435 440 445

Leu Gly Gly Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Val Glu  
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Ala Tyr Lys

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<222> (1)..(18)  
<223> Oligonucleotide primer 1A for Chlamydomonas reinhardtii

<400> 15  
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<210> 16  
<211> 19  
<212> DNA  
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<400> 16  
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<210> 17

<211> 17  
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<223> Oligonucleotide primer 2A for Chlamydomonas reinhardtii

<400> 17  
actttgtctg gtgctcc 17

<210> 18  
<211> 17  
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<223> Oligonucleotide primer 2B for Chlamydomonas reinhardtii

<400> 18  
tggatcgctt tgctcag 17

<210> 19  
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<223> Strain RS-3

<220>  
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tccatcccga ttccatccgc tcctcctccc ccaccttagac tgtctaccgt ctaccagtt 180  
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tgacgctgtc gtacccgctg agcgccgtgc gygaggagcg caaggcctcg gacgggtccg 360  
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 <211> 18  
 <212> DNA  
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<220>  
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 <223> Oligonucleotide primer 3A for Chlamydomonas reinhardtii

<400> 20  
ttccacgtct tccacctg 18

<210> 21  
<211> 17  
<212> DNA  
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<223> Oligonucleotide primer 3B for Chlamydomonas reinhardtii

<400> 21  
ctaggatcta gcccatc 17

<210> 22  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
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<223> Oligonucleotide primer 4A for Chlamydomonas reinhardtii

<400> 22  
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<210> 23  
<211> 18  
<212> DNA  
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<220>  
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<223> Oligonucleotide primer 4B for Chlamydomonas reinhardtii

<400> 23  
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<400> 24  
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17